

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/975,123

DATE: 11/01/2001
TIME: 08 41:48

Input Set : A:\ES.txt
Output Set: N:\CRF3\11012001\I975123.raw

3 <110> APPLICANT: Susan M. Freier
6 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF INSULIN-LIKE GROWTH FACTOR BINDING
PROTEIN 5
7 EXPRESSION
9 <130> FILE REFERENCE: RTS-0253
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/975,123
C--> 11 <141> CURRENT FILING DATE: 2001-10-09
11 <160> NUMBER OF SEQ ID NOS: 43
14 <210> SEQ ID NO: 1
15 <211> LENGTH: 20
16 <212> TYPE: DNA
17 <213> ORGANISM: Artificial Sequence
19 <220> FEATURE:
31 <223> OTHER INFORMATION: Antisense Oligonucleotide
33 <400> SEQUENCE: 1
24 tccgtcatacg ctcctcaggg 20
27 <210> SEQ ID NO: 2
28 <211> LENGTH: 20
29 <212> TYPE: DNA
30 <213> ORGANISM: Artificial Sequence
32 <220> FEATURE:
34 <223> OTHER INFORMATION: Antisense Oligonucleotide
36 <400> SEQUENCE: 2
37 atqcattctg cccccaagga 20
40 <210> SEQ ID NO: 3
41 <211> LENGTH: 1612
42 <212> TYPE: DNA
43 <213> ORGANISM: Homo sapiens
45 <220> FEATURE:
47 <220> FEATURE:
48 <221> NAME/KEY: CDS
49 <222> LOCATION: (44)...(862)
51 <100> SEQUENCE: 3
52 ctgttcgtcc ccaaccccaq qtaaaqqqqq cqactaaqaq aaq atq qtq ttq ctc 55
53 Met Val Leu Leu
54 |
55 aac qcq qtc ctc ctq ctq qcc qcc tat qcq qqg ccc qcc caq aqc 103
56 Thr Ala Val Leu Leu Ala Ala Tyr Ala Gly Pro Ala Gln Ser
57 5 10 15 20
60 ctq ggc tcc ttc qtg cac tgc gag ccc tgc qac gaa aaa gcc ctc tcc 151
61 Leu Gly Ser Phe Val His Cys Glu Pro Cys Asp Glu Lys Ala Leu Ser
62 25 30 35
64 atq tgc ccc ccc aqc ccc ctq qqc tgc qag ctq gtc aaq qaq ccc qqc 199
65 Met Cys Pro Pro Ser Pro Leu Gly Cys Glu Leu Val Lys Glu Pro Gly

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72	gtc	tac	acc	gag	cgc	tgc	gcc	cag	ggg	ctg	cgc	tgc	ctc	ccc	cgg	cag	295
73	Val	Tyr	Thr	Glu	Arg	Cys	Ala	Gln	Gly	Leu	Arg	Cys	Leu	Pro	Arg	Gln	
74	70			75						80							
76	gac	gag	gag	aag	cgc	ctg	cac	gcc	ctg	cac	ggc	cgc	ggg	gtt	tgc	343	
77	Asp	Glu	Glu	Lys	Pro	Leu	His	Ala	Leu	Leu	His	Gly	Arg	Gly	Val	Cys	
78	85			90						95				100			
80	ctc	aac	qaa	aag	agc	tac	cgc	gag	caa	gtc	aag	atc	gag	aga	qac	ttc	391
81	Leu	Asn	Glu	Lys	Ser	Tyr	Arg	Glu	Gln	Val	Lys	Ile	Glu	Arg	Asp	Ser	
82				105						110				115			
84	cgt	gag	cac	gag	gag	ccc	acc	acc	tct	gag	atg	gcc	gag	gag	acc	ttc	439
85	Arg	Glu	His	Glu	Glu	Pro	Thr	Thr	Ser	Glu	Met	Ala	Glu	Glu	Thr	Tyr	
86				120						125				130			
88	tcc	ccc	aag	atc	ttc	cgg	ccc	aaa	cac	acc	cgc	atc	tcc	qaq	ctg	aag	487
89	Ser	Pro	Lys	Ile	Phe	Arg	Pro	Lys	His	Thr	Arg	Ile	Ser	Glu	Leu	Lys	
90				135						140				145			
92	gtc	gaa	gca	gtg	aag	aaq	aaq	gac	cgc	aaq	535						
93	Ala	Glu	Ala	Val	Lys	Lys	Asp	Arg	Arg	Lys	Lys	Leu	Thr	Gln	Ser	Lys	
94				150						155				160			
96	ttt	gtc	ggg	gqa	gcc	gag	aac	act	gcc	cac	ccc	cgg	atc	atc	tct	gca	583
97	Phe	Val	Gly	Gly	Ala	Glu	Asn	Thr	Ala	His	Pro	Arg	Ile	Ile	Ser	Ala	
98	165			170						175				180			
100	cct	gag	atg	aga	cag	gag	tct	gag	cag	ggc	ccc	tgc	cgc	aga	cac	atg	631
101	Pro	Glu	Met	Arg	Gln	Glu	Ser	Glu	Gln	Gly	Pro	Cys	Arg	Arg	His	Met	
102				185						190				195			
104	qag	gct	tcc	ctg	cag	gag	ctc	aaa	gcc	agc	cca	cgc	atg	gtg	ccc	cgt	679
105	Glu	Ala	Ser	Leu	Gln	Glu	Leu	Lys	Ala	Ser	Pro	Arg	Met	Val	Pro	Arg	
106				200						205				210			
108	qct	gtg	tac	ctg	ccc	aat	tgt	qac	cgc	aaa	qga	ttc	tac	aaq	aga	aag	727
109	Ala	Val	Tyr	Leu	Pro	Asn	Cys	Asp	Arg	Lys	Gly	Phe	Tyr	Lys	Arg	Lys	
110				215						220				225			
112	cag	tgc	aaa	cct	tcc	cgt	ggc	cgc	aag	cgt	ggc	atc	tgc	tgg	tgc	gtg	775
113	Gln	Cys	Lys	Pro	Ser	Arg	Gly	Arg	Lys	Arg	Gly	Ile	Cys	Trp	Cys	Val	
114				230						235				240			
116	qac	aag	tac	ggg	atg	aag	ctg	cca	ggc	atg	qag	tac	gtt	gac	ggg	qac	823
117	Asp	Lys	Tyr	Gly	Met	Lys	Leu	Pro	Gly	Met	Glu	Tyr	Val	Asp	Gly	Asp	
118	245			250						255				260			
120	ttt	caq	tgc	cac	acc	ttc	qac	agc	agc	aac	qtt	qaq	tqa	tgcgtcccc		872	
121	Phe	Gln	Cys	His	Thr	Phe	Asp	Ser	Ser	Asn	Val	Glu					
122				265						270							
124	ccccaaaccttt	cccttcaacc	ccccaaacctt	cccccaccc	caqcccccac	ccccacccac	cccccaccc	932									
126	cccccccaqqac	cccccaccc	992														
128	ggaaaactggag	1052															
130	gatgcaaaaaa	1112															
132	ggatcaacaa	1172															
134	tgtatcaacaa	1232															
136	aggacatqca	1292															
138	qqqaqaqgtq	1352															
140	tttcccccaqqa	1412															
																1472	

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144	cttttacctg	ggcagagtgt	tgtctctccc	caaatttata	aaaactaaaa	tgcattccat	1532
146	tcctctgaaa	gaaaaacaaa	tctataattt	agtqatatta	aatagaqaaq	ttttcqqaag	1592
148	cgatctgtg	aatatgaaaat					1612
151	<210>	SEQ ID NO:	4				
152	<211>	LENGTH:	19				
153	<212>	TYPE:	DNA				
154	<213>	ORGANISM:	Artificial Sequence				
156	<220>	FEATURE:					
158	<223>	OTHER INFORMATION:	PCR Primer				
160	<400>	SEQUENCE:	4				
161	ccaaaaacacac	ccgcacatcc					19
164	<210>	SEQ ID NO:	5				
165	<211>	LENGTH:	22				
166	<212>	TYPE:	DNA				
167	<213>	ORGANISM:	Artificial Sequence				
169	<220>	FEATURE:					
171	<223>	OTHER INFORMATION:	PCR Primer				
173	<400>	SEQUENCE:	5				
174	tggactggg	tcaatttttt	tc				22
177	<210>	SEQ ID NO:	6				
178	<211>	LENGTH:	26				
179	<212>	TYPE:	DNA				
180	<213>	ORGANISM:	Artificial Sequence				
182	<220>	FEATURE:					
184	<223>	OTHER INFORMATION:	PCR Probe				
186	<400>	SEQUENCE:	6				
187	aaatgtaaagc	atgttaagaag	gaccgc				26
190	<210>	SEQ ID NO:	7				
191	<211>	LENGTH:	19				
192	<212>	TYPE:	DNA				
193	<213>	ORGANISM:	Artificial Sequence				
195	<220>	FEATURE:					
197	<223>	OTHER INFORMATION:	PCR Primer				
199	<400>	SEQUENCE:	7				
200	aaatgtaaag	atgttttttt	tcggagtc				19
203	<210>	SEQ ID NO:	8				
204	<211>	LENGTH:	20				
205	<212>	TYPE:	DNA				
206	<213>	ORGANISM:	Artificial Sequence				
208	<220>	FEATURE:					
210	<223>	OTHER INFORMATION:	PCR Primer				
212	<400>	SEQUENCE:	8				
213	aaatgtaaat	atgttttttt	tcggatcc				20
216	<210>	SEQ ID NO:	9				
217	<211>	LENGTH:	20				
218	<212>	TYPE:	DNA				
219	<213>	ORGANISM:	Artificial Sequence				
221	<220>	FEATURE:					
222	<223>	OTHER INFORMATION:	PCR Probe				

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225 <400 · SEQUENCE: 9
226 caagettccg gtttctcagcc 20
229 <210 · SEQ ID NO: 10
230 <211 · LENGTH: 1722
231 <212 · TYPE: DNA
232 <213 · ORGANISM: Homo sapiens
234 <220 · FEATURE:
236 <220 · FEATURE:
237 <221 · NAME/KEY: CDS
238 <222 · LOCATION: (752)...(1570)
240 <400 · SEQUENCE: 10
241 qjqqaaaaga gctaggaaag aqctgcaaag cagtgtggc tttttccctt tttttgtcc 60
243 ttttcaattac ccctctccg ttttccaccc ttcggact tcgcgttagaa cctgcqaatt 120
245 tcgaaaggagga ggtggcaaag tgggagaaaa gaggtgttag ggtttggggt tttttgttt 180
247 ttgtttttgt ttttaattt cttgatttca acattttcc ecaccctetc ggctgcagecc 240
249 aacgcctttt acctgttctg cggcgcgcgcg caccqctqcc aqctqaqqgt tagaaagcgg 300
251 qqtgtatttt agatttaag caaaaatttt aaagataaaat ccatttttct ccccaacccc 360
253 caacqccatc tccactgcat cegatctcat tatttcggc gttgttggg ggtgaacaat 420
255 ttgtgtggcatt tttttccctt ataattctga cccgttcagg ttgtggggtt ttcggcct 480
257 cccgtcaactg cgtgcacctg ggcgtgcctt gttttccca acctgttgcg aggcttaat 540
259 ttttgcactt gggacctgtt cgcaggcacc ccagccctcc acctctctt acattttgc 600
261 aagtgtctgg gggagggcactgtctacc tgccagaaat tttaaaacaa aaacaaaaac 660
263 aaaaaaatct cggggggccc ttgtggccc ttatccctg cactctgtt ctcgtcccc 720
265 accccgaggt aaaggggggcg actaagagaa g atg gtg ttg ctc acc gcg gtc 772
266 Met Val Leu Leu Thr Ala Val
267 1 5
269 ctc ctg ctg ctg gcc gcc tat gcg ggg ccc gcc cag agc ctg ggc tcc 820
270 Leu Leu Leu Ala Ala Tyr Ala Gly Pro Ala Gln Ser Leu Gly Ser
271 10 15 20
273 ttc qtg cac tgc gag ccc tgc gac gag aaa gcc ctc tcc atq tgc ccc 868
274 Phe Val His Cys Glu Pro Cys Asp Glu Lys Ala Leu Ser Met Cys Pro
275 25 30 35
277 ccc agc ccc ctg ggc tgc gag ctg gtc aag gag ccc ggc tgc ggc tgc 916
278 Pro Ser Pro Leu Gly Cys Glu Leu Val Lys Glu Pro Gly Cys Gly Cys
279 40 45 50 55
281 tgc atq acc tgc gcc ctg gcc gag ggg cag tgc tgc ggc qtc tac acc 964
282 Cys Met Thr Cys Ala Leu Ala Glu Gly Gln Ser Cys Gly Val Tyr Thr
283 60 65 70
285 qaq cgc tgc qcc caq gqq ctg cgc tgc ctc ccc cgg cag qac qaq qaq 1022
286 Glu Arg Cys Ala Gln Gly Leu Arg Cys Leu Pro Arg Gln Asp Glu Glu
287 75 80 85
289 aaq ccc ctg cac qcc ctg cac qgc ccc qcc qqq qtt tgc ctc aac qaa 1060
290 Lys Pro Leu His Ala Leu His Gly Arg Gly Val Cys Leu Asn Glu
291 90 95 100
293 aaq aqc tac cgc qaq caa gtc aqg atc qaq aqa qac tcc cgt qaq cac 1108
294 Lys Ser Tyr Arg Glu Gln Val Lys Ile Glu Arg Asp Ser Arg Glu His
295 105 110 115
297 qaq qaq ccc acc acc tct qaq atq gcc qaq qaq acc tac tcc ccc aqg 1156
298 116 121 126 131 136 Met Ala Glu Glu Thr Tyr Ser Pro Lys

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/975,123

DATE 11/01/2001

TIME 08:41 49

Input Set A:\ES.txt

Output Set N:\CRF3\11012001\1975123.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date